

Serial No.: 09/782,171

Filed: February 12, 2001

REMARKS

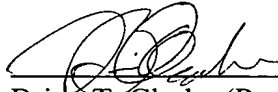
The present amendments correct unintended dependencies in Claims 2 and 4. No new matter is presented by these amendments, and entry into the instant application is respectfully requested. Attached hereto is a "Marked-Up Version" showing the amendments, and an "Appendix of Pending Claims" for the Examiner's convenience.

It is believed that all claims are in condition for allowance and an early notification thereof is kindly solicited.

Respectfully submitted,

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Date: August 13, 2001



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Marked-Up Version

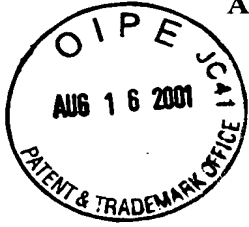
2. The method according to Claim 1[, 11] further comprising:
 - (c) storing a first genomic product report for each of said at least two genomics products in a customer report database, wherein said first genomic product report contains searchable genomic product data.

4. The method according to Claim 1, [11] 2, or 3, wherein said at least one genomic product is selected from the group consisting of a nucleic acid clone, a genotypically modified cell, a transgenic genotypically modified animal.

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1. A method for providing integrated genomic services comprising:
 - (a) receiving a first request from a customer, wherein said request comprises a first nucleic acid sequence, and an order for at least two genomics products; and
 - (b) utilizing said nucleic acid sequence to provide said at least two genomics services or products.
2. The method according to Claim 1 further comprising:
 - (c) storing a first genomic product report for each of said at least two genomics products in a customer report database, wherein said first genomic product report contains searchable genomic product data.
3. The method according to Claim 2 further comprising:
 - (d) receiving a second request from said customer; wherein said request comprises a second order for at least one genomics product, and a second nucleic acid sequence;
 - (e) comparing said second order and/or said second nucleic acid sequence against said genomic product report to determine if said second request or nucleic acid sequence is redundant.
4. The method according to Claim 1, 2 or 3, wherein said at least one genomic product is selected from the group consisting of a nucleic acid clone, a genotypically modified cell, a transgenic genotypically modified animal.
5. The method according to Claim 4, wherein said genotypically modified cell line comprises a plurality of cell lines, wherein at least two of said cell lines have a different genotypic modification
6. The method according to Claim 4, wherein said nucleic acid clone comprises a plurality of clones representing at least a subset of a gene family.

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7. The method according to Claim 4, wherein said at least one genomic product is made by a recombinase mediated process.

8. The method according to Claim 7, wherein said recombinase mediated process is selected from the group consisting of:

(i) cloning a nucleic acid by contacting a nucleic acid library with first and second substantially complementary single-stranded targeting polynucleotides and a recombinase, wherein said first single-stranded targeting polynucleotide comprises said first nucleic acid sequence or a homologue thereof, and isolating said nucleic acid;

(ii) producing a modified cell with a targeted sequence modification by introducing into a cell first and second substantially complementary single-stranded targeting polynucleotides and a recombinase, wherein said first single-stranded targeting polynucleotide comprises said first nucleic acid sequence or a homologue thereof, and further comprises a homology clamp substantially corresponding to or substantially complementary to a pre-selected target DNA sequence, and identifying a cell having said targeted sequence modification; and

(iii) producing a transgenic animal with a modified preselected DNA sequence, by introducing into a zygote first and second substantially complementary single-stranded targeting polynucleotides and a recombinase, wherein said first single-stranded targeting polynucleotide comprises said first nucleic acid sequence or a homologue thereof and further comprises a homology clamp substantially corresponding to or substantially complementary to a pre-selected wild-type target DNA sequence, wherein said pre-selected wild-type target DNA sequence is modified by homologous recombination with at least one of said first or second substantially complementary single-stranded targeting polynucleotides, and generating said transgenic non-human mammal from said zygote.

9. A method for providing integrated genomics services comprising:

(a) receiving a first request from a customer comprising a first nucleic acid sequence and an order for at least one first genomic product or service;

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- (b) receiving a second request from the same or different customer comprising a second nucleic acid sequence and an order for at least one second genomic product or service; and
- (c) utilizing said first and said second nucleic acid sequences to provide said first and said second genomic product or service to said customers.

10. A method for providing an integrated genomic service comprising:

- (a) receiving a first request from a customer comprising a first nucleic acid sequence and an order for at least one genomic product or service; and
- (b) utilizing said first nucleic acid sequence in a recombinase mediated process to for said at least one genomic product.

11. A computer program for integrating the provision of genomic services and products comprising:

a request receiving module including instructions for:

- (a) receiving a first request from a customer, wherein said request comprises a first nucleic acid sequence, and an order for at least two genomics products, and
- (b) processing said request to obtain said at least two genomics products.

12. The computer program according to Claim 11, wherein said processing step further comprises:

- (i) saving said first request in as request database,
- (ii) searching databases to determine if said first request or said first nucleic acid is wholly or partially redundant to information within said databases, and
- (iii) updating said first request if any additional information is found in step (ii)